**BIOTECHNOLOGY
SYSTEMS
BRANCH**
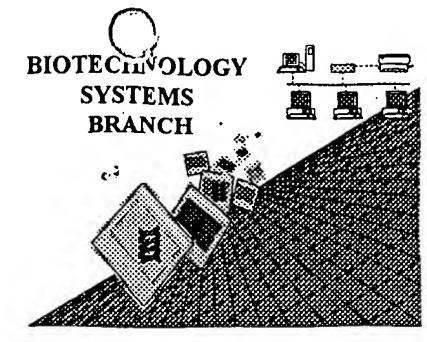
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/265,540P_

Source: _1647_

Date Processed by STIC: _3/27/2001_

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/265,5400 |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1647

RAW SEQUENCE LISTING   DATE: 03/27/2001
PATENT APPLICATION: US/09/265,540D   TIME: 10:50:04

Input Set : A:\804k.app
Output Set: N:\CRF3\03272001\I265540D.raw

Does Not Comply
Corrected Diskette Needed

see pp. 2-3,

```
 3 <110> APPLICANT: Parham, Christi L.
 4         Moore, Kevin W.
 5         Murgolo, Nicholas J.
 6         Bazan, J. Fernando
 8 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
10 <130> FILE REFERENCE: DX0804K
12 <140> CURRENT APPLICATION NUMBER: 09/265,540D
13 <141> CURRENT FILING DATE: 1999-03-08
15 <160> NUMBER OF SEQ ID NOS: 6
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1381
21 <212> TYPE: DNA
22 <213> ORGANISM: primate
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (132)..(1064)
28 <220> FEATURE:
29 <221> NAME/KEY: unsure
30 <222> LOCATION: (567)
31 <223> OTHER INFORMATION: n at position 567; n may be A, C, G, or T;
32         translated amino acid depends on genetic code
34 <220> FEATURE:
35 <221> NAME/KEY: unsure
36 <222> LOCATION: (573)
37 <223> OTHER INFORMATION: n at position 573; n may be A, C, G, or T;
38         translated amino acid depends on genetic code
40 <220> FEATURE:
41 <221> NAME/KEY: unsure
42 <222> LOCATION: (1336)
43 <223> OTHER INFORMATION: n at position 1336; n may be A,C, G, or T;
44         translated amino acid depends on genetic code
46 <220> FEATURE:
47 <221> NAME/KEY: unsure
48 <222> LOCATION: (1342)
49 <223> OTHER INFORMATION: n at position 1342; n may be A, C, G, or T;
50         translated amino acid depends on genetic code
52 <220> FEATURE:
53 <221> NAME/KEY: unsure
54 <222> LOCATION: (1369)
55 <223> OTHER INFORMATION: n at position 1369; n may be A, C, G, or T;
56         translated amino acid depends on genetic code
58 <400> SEQUENCE: 1
59 tcgacccacg cgtccgcgct gcgactcaga cctcagctcc aacatatgca ttctgaagaa 60
61 agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaact 120
63 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca  170
64                Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr
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RAW SEQUENCE LISTING   DATE: 03/27/2001
PATENT APPLICATION: US/09/265,540D   TIME: 10:50:04

                     Input Set : A:\804k.app
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65                  1              5                  10
67 agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca   218
68 Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr
69      15              20                  25
71 gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca   266
72 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
73 30                  35              40                  45
75 acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga   314
76 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
77          50                  55              60
79 gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg   362
80 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
81          65              70                  75
83 tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa   410
84 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
85          80                  85              90
87 ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac   458
88 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
89      95                  100             105
91 aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc   506
92 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
93 110                 115             120                 125
95 atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct   554
96 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
97              130                 135             140
```
W --> 99 ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag   602
W --> 100 Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu
```
101                 145             150                 155
103 gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag   650
```
W --> 104 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu
```
105         160             165                 170
107 cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca   698
108 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
109 175                 180             185
111 gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc   746
112 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
113 190                 195             200                 205
115 cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca   794
116 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr
117             210             215                 220
119 gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg   842
120 Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu
121             225             230                 235
123 ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc   890
124 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe
125         240             245                 250
127 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg   938
128 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val
129         255                 260             265
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(handwritten annotation: move amino acids directly under respective codon)

RAW SEQUENCE LISTING   DATE: 03/27/2001
PATENT APPLICATION: US/09/265,540D   TIME: 10:50:04

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Output Set: N:\CRF3\03272001\I265540D.raw

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131 gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc  986
132 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
133 270                     275                 280                 285
135 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct 1034
136 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser
137             290                 295                 300
139 cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca   1084
140 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
141             305                 310
143 ggtgaagccg agaacctggt ctgcatgaca tggaaaccat gaggggacaa gttgtgtttc 1144
145 tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgtc tacaagtcta 1204
147 gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg 1264
149 gwtgtgacct ctagactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga 1324
151 cttcatccct tnggtccnaa gttttctcat ctgtaatggg ggatncctac aaaactg    1381
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 311
156 <212> TYPE: PRT
157 <213> ORGANISM: primate
159 <400> SEQUENCE: 2
160 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe
161 1               5                   10                  15
163 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val
164             20                  25                  30
166 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met
167         35                  40                  45
169 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
170     50                  55                  60
172 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
173 65                  70                  75                  80
175 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
176             85                  90                  95
178 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
179             100                 105                 110
181 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
182             115                 120                 125
184 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
185         130                 135                 140
187 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
188 145                 150                 155                 160
190 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala
191             165                 170                 175
193 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
194             180                 185                 190
196 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
197         195                 200                 205
199 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
200         210                 215                 220
202 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
203 225                 230                 235                 240
```

W--> 187
W--> 190
W--> 199
W--> 202

```
205 Val Gly Phe Met Leu Ile Leu Val Val Pro Leu Phe Val Trp Lys
206                 245                 250                 255
208 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Leu Pro
209             260                 265                 270
211 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
212         275                 280                 285
214 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu
215     290                 295                 300
217 Leu Leu Arg Ala Trp Ile Ser
218 305                 310
221 <210> SEQ ID NO: 3
222 <211> LENGTH: 1244
223 <212> TYPE: DNA
224 <213> ORGANISM: primate
226 <220> FEATURE:
227 <221> NAME/KEY: CDS
228 <222> LOCATION: (2)..(694)
230 <220> FEATURE:
231 <221> NAME/KEY: unsure
232 <222> LOCATION: (193)
234 <400> SEQUENCE: 3
235 c cgg gtc gac cca cgc gtc cgc ctg gtt tcc ccc tgg ctg aca gtg cct 49
236   Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
237   1               5                   10                  15
239 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc  97
240 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
241             20                  25                  30
243 tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc 145
244 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
245         35                  40                  45
247 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193
248 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
249     50                  55                  60
251 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241
252 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
253 65                  70                  75                  80
255 tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289
256 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
257             85                  90                  95
259 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc 337
260 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
261             100                 105                 110
263 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385
264 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
265         115                 120                 125
267 aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg 433
268 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
269     130                 135                 140
271 gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc 481
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RAW SEQUENCE LISTING   DATE: 03/27/2001
PATENT APPLICATION: US/09/265,540D   TIME: 10:50:04

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Output Set: N:\CRF3\03272001\I265540D.raw

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272 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
273 145             150             155             160
275 ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc   529
276 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
277             165             170             175
279 gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac   577
280 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
281             180             185             190
283 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt   625
284 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
285             195             200             205
287 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc   673
288 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
289             210             215             220
291 caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggct ctgagccgag   724
292 Gln Asn Ser Gly Ala Val Cys
293             225             230
295 gaagctgctg atgtccatgt cagcacttta tggaatccgg tcctccattt tcctgtcccc 784
297 aaaaggcccg tcagtgcctg tgaagatgta acgggtctca tggggcgac aagcttattg 844
299 atttttttct tcaaactaag agtttctaa tcatacgcgt ttttagaata attctacaga 904
301 tatgtccccg aaagattaag atttctctta aacactaaaa agacatgtaa ttatttgtta 964
303 gcaaatgggc gtctggcacg cctctgacac tttttcgtca gcagccagga cacgaggtcc 1024
305 cctccttgat gaagccctc gggcagacca tgtcacctgt cccagcctgc cccaagaagg 1084
307 gacattaagt ggcccttctt catatccaaa cacctggctt gaaatgtgat tagccctgta 1144
309 aatagtttca cagagattaa gccttttttt cccccaagtt aggaataaaa gactataatt 1204
311 aactttttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa                         1244
314 <210> SEQ ID NO: 4
315 <211> LENGTH: 231
316 <212> TYPE: PRT
317 <213> ORGANISM: primate
319 <400> SEQUENCE: 4
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321 1               5               10              15
323 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
324             20              25              30
326 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
327             35              40              45
329 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
330             50              55              60
332 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
333 65              70              75              80
335 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
336             85              90              95
338 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
339             100             105             110
341 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
342             115             120             125
344 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
345 130             135             140
```

W --> (handwritten annotation at line 329, with circled "Xaa"): *see item 10*

VERIFICATION SUMMARY   DATE: 03/27/2001
PATENT APPLICATION: US/09/265,540D   TIME: 10:50:05

Input Set : A:\804k.app
Output Set: N:\CRF3\03272001\I265540D.raw

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L:99  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:187 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:187 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:187 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:187 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:187 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:190 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:190 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:190 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:190 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:199 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:199 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:199 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:199 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:202 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
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L:202 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:248 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:248 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:329 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:329 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:329 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
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L:329 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
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